

SEQUENCE LISTING

<110> Susan Murray
Jacqueline Wyatt

<120> ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA RECEPTOR II
EXPRESSION

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Ile Val Leu Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln
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Pro Pro Leu Gly Val Ala Ile Ser Val Ile Ile Ile Phe Tyr Cys Tyr				
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 Arg Phe Ala Glu Val Tyr Lys Ala Lys Leu Lys Gln Asn Thr Ser Glu
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Arg Gly Leu Trp Pro Leu His Ile Val Leu Trp Thr Arg Ile Ala Ser
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Thr Ile Pro Pro His Val Pro Lys Ser Asp Val Glu Met Glu Ala Gln
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Lys Asp Ala Ser Ile His Leu Ser Cys Asn Arg Thr Ile His Pro Leu
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Lys His Phe Asn Ser Asp Val Met Ala Ser Asp Asn Gly Gly Ala Val
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Lys Leu Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Leu Ser Thr Cys
75 80 85

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Asp Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ala Ile Cys
90 95 100

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105 110 115

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Asn Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys Leu Thr Tyr His
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Gly Phe Thr Leu Glu Asp Ala Ala Ser Pro Lys Cys Val Met Lys Glu

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Lys Lys Arg Ala Gly Glu Thr Phe Phe Met Cys Ala Cys Asn Met Glu				
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375 380 385 390

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Thr Pro Cys Gly Arg Pro Lys Met Pro Ile Val His Arg Asp Leu Lys
395 400 405

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 Val Arg Glu His Pro Cys Val Glu Ser Met Lys Asp Ser Val Leu Arg
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tccggagagg gcgcggcgcg gagcgcagcc aggggtccgg gaaggcgccg tccgtgcgct	300
gggggctcgg tctatgacga gcagcgggggt ctgcc atg ggt cgg ggg ctg ctc	353
Met Gly Arg Gly Leu Leu	
1 5	
agg ggc ctg tgg ccg ctg cac atc gtc ctg tgg acg cgt atc gcc agc	401
Arg Gly Leu Trp Pro Leu His Ile Val Leu Trp Thr Arg Ile Ala Ser	
10 15 20	
acg atc cca ccg cac gtt cag aag tcg gtt aat aac gac atg ata gtc	449
Thr Ile Pro Pro His Val Gln Lys Ser Val Asn Asn Asp Met Ile Val	
25 30 35	
act gac aac aac ggt gca gtc aag ttt cca caa ctg tgt aaa ttt tgt	497
Thr Asp Asn Asn Gly Ala Val Lys Phe Pro Gln Leu Cys Lys Phe Cys	
40 45 50	
gat gtg aga ttt tcc acc tgt gac aac cag aaa tcc tgc atg agc aac	545
Asp Val Arg Phe Ser Thr Cys Asp Asn Gln Lys Ser Cys Met Ser Asn	
55 60 65 70	
tgc agc atc acc tcc atc tgt gag aag cca cag gaa gtc tgt gtg gct	593
Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala	
75 80 85	
gta tgg aga aag aat gac gag aac ata aca cta gag aca gtt tgc cat	641
Val Trp Arg Lys Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His	
90 95 100	
gac ccc aag ctc ccc tac cat gac ttt att ctg gaa gat gct gct tct	689
Asp Pro Lys Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser	
105 110 115	
cca aag tgc att atg aag gaa aaa aaa aag cct ggt gag act ttc ttc	737

Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe
 120 125 130

atg tgt tcc tgt agc tct gat gag tgc aat gac aac atc atc ttc tca 785
 Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser
 135 140 145 150

gaa gaa tat aac acc agc aat cct gac ttg ttg cta gtc ata ttt caa 833
 Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu Leu Leu Val Ile Phe Gln
 155 160 165

gtg aca ggc atc agc ctc ctg cca cca ctg gga gtt gcc ata tct gtc 881
 Val Thr Gly Ile Ser Leu Leu Pro Pro Leu Gly Val Ala Ile Ser Val
 170 175 180

atc atc atc ttc tac tgc tac cgc gtt aac cgg cag cag aag ctg agt 929
 Ile Ile Ile Phe Tyr Cys Tyr Arg Val Asn Arg Gln Gln Lys Leu Ser
 185 190 195

tca acc tgg gaa acc ggc aag acg cgg aag ctc atg gag ttc agc gag 977
 Ser Thr Trp Glu Thr Gly Lys Thr Arg Lys Leu Met Glu Phe Ser Glu
 200 205 210

cac tgt gcc atc atc ctg gaa gat gac cgc tct gac atc agc tcc acg 1025
 His Cys Ala Ile Ile Leu Glu Asp Asp Arg Ser Asp Ile Ser Ser Thr
 215 220 225 230

tgt gcc aac aac atc aac cac aac aca gag ctg ctg ccc att gag ctg 1073
 Cys Ala Asn Asn Ile Asn His Asn Thr Glu Leu Leu Pro Ile Glu Leu
 235 240 245

gac acc ctg gtg ggg aaa ggt cgc ttt gct gag gtc tat aag gcc aag 1121
 Asp Thr Leu Val Gly Lys Gly Arg Phe Ala Glu Val Tyr Lys Ala Lys
 250 255 260

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 Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu Thr Val Ala Val Lys Ile
 265 270 275

ttt ccc tat gag gag tat gcc tct tgg aag aca gag aag gac atc ttc 1217
Phe Pro Tyr Glu Glu Tyr Ala Ser Trp Lys Thr Glu Lys Asp Ile Phe
280 285 290

tca gac atc aat ctg aag cat gag aac ata ctc cag ttc ctg acg gct 1265
Ser Asp Ile Asn Leu Lys His Glu Asn Ile Leu Gln Phe Leu Thr Ala
295 300 305 310

gag gag cgg aag acg gag ttg ggg aaa caa tac tgg ctg atc acc gcc 1313
Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln Tyr Trp Leu Ile Thr Ala
315 320 325

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Phe His Ala Lys Gly Asn Leu Gln Glu Tyr Leu Thr Arg His Val Ile
330 335 340

agc tgg gag gac ctg cgc aag ctg ggc agc tcc ctc gcc cgg ggg att 1409
Ser Trp Glu Asp Leu Arg Lys Leu Gly Ser Ser Leu Ala Arg Gly Ile
345 350 355

gct cac ctc cac agt gat cac act cca tgt ggg agg ccc aag atg ccc 1457
Ala His Leu His Ser Asp His Thr Pro Cys Gly Arg Pro Lys Met Pro
360 365 370

atc gtg cac agg gac ctc aag agc tcc aat atc ctc gtg aag aac gac 1505
Ile Val His Arg Asp Leu Lys Ser Ser Asn Ile Leu Val Lys Asn Asp
375 380 385 390

cta acc tgc tgc ctg tgt gac ttt ggg ctt tcc ctg cgt ctg gac cct 1553
Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu Ser Leu Arg Leu Asp Pro
395 400 405

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Thr Leu Ser Val Asp Asp Leu Ala Asn Ser Gly Gln Val Gly Thr Ala
410 415 420

aga tac atg gct cca gaa gtc cta gaa tcc agg atg aat ttg gag aat 1649
Arg Tyr Met Ala Pro Glu Val Leu Glu Ser Arg Met Asn Leu Glu Asn
425 430 435

gct gag tcc ttc aag cag acc gat gtc tac tcc atg gct ctg gtg ctc 1697
Ala Glu Ser Phe Lys Gln Thr Asp Val Tyr Ser Met Ala Leu Val Leu
440 445 450

tgg gaa atg aca tct cgc tgt aat gca gtg gga gaa gta aaa gat tat 1745
Trp Glu Met Thr Ser Arg Cys Asn Ala Val Gly Glu Val Lys Asp Tyr
455 460 465 470

gag cct cca ttt ggt tcc aag gtg cgg gag cac ccc tgt gtc gaa agc 1793
Glu Pro Pro Phe Gly Ser Lys Val Arg Glu His Pro Cys Val Glu Ser
475 480 485

atg aag gac aac gtg ttg aga gat cga ggg cga cca gaa att ccc agc 1841
Met Lys Asp Asn Val Leu Arg Asp Arg Gly Arg Pro Glu Ile Pro Ser
490 495 500

ttc tgg ctc aac cac cag ggc atc cag atg gtg tgt gag acg ttg act 1889
Phe Trp Leu Asn His Gln Gly Ile Gln Met Val Cys Glu Thr Leu Thr
505 510 515

gag tgc tgg gac cac gac cca gag gcc cgt ctc aca gcc cag tgt gtg 1937
Glu Cys Trp Asp His Asp Pro Glu Ala Arg Leu Thr Ala Gln Cys Val
520 525 530

gca gaa cgc ttc agt gag ctg gag cat ctg gac agg ctc tcg ggg agg 1985
Ala Glu Arg Phe Ser Glu Leu Glu His Leu Asp Arg Leu Ser Gly Arg
535 540 545 550

agc tgc tcg gag gag aag att cct gaa gac ggc tcc cta aac act acc 2033
Ser Cys Ser Glu Glu Lys Ile Pro Glu Asp Gly Ser Leu Asn Thr Thr
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gaggatgcag tgagcg atg ata cta cca ctg cat aac ctg ggc aat gga gtg 952
Met Ile Leu Pro Leu His Asn Leu Gly Asn Gly Val
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agg tcc cat aac ttt tct ttt ctt tac ttt att ctg gaa gat gct gct 1000
Arg Ser His Asn Phe Ser Phe Leu Tyr Phe Ile Leu Glu Asp Ala Ala
15 20 25
tct cca aag tgc att atg aag gaa aaa aaa aag cct ggt gag act ttc 1048
Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe
30 35 40
ttc atg tgt tcc tgt agc tct gat gag tgc aat gac aac atc atc ttc 1096
Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe
45 50 55 60
tca gaa gaa tat aac acc agc aat cct gac ttg ttg cta gtc ata ttt 1144
Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu Leu Leu Val Ile Phe
65 70 75
caa gtg aca ggc atc agc ctc ctg cca cca ctg gga gtt gcc ata tct 1192
Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu Gly Val Ala Ile Ser
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acttattttt attctatgca ttgnttgctt ttacataaa taaaatgttt attagattga 240

ataaagcaaa atactcaggt gagcatcctg cctcctgttc ccattcctag tagctaaatc 300

catttgcctc atttggttat ttgcaattt atgcagaaaa cgtcaccaag taaataatct 360

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